

PATENTS

JC828 U.S. PTO  
10/066496  
01/31/02

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

<b>Applicant(s):</b>	Eldon Emberly, et al.	<b>Examiner:</b>	Unassigned
<b>Serial No:</b>	Unassigned	<b>Art Unit:</b>	Unassigned
<b>Filed:</b>	Herewith	<b>Docket:</b>	15157
<b>For:</b>	METHOD OF IDENTIFYING DESIGNABLE PROTEIN BACKBONE CONFIGURATIONS	<b>Dated:</b>	January 31, 2002

Assistant Commissioner for Patents  
Washington, D.C. 20231

**INFORMATION DISCLOSURE STATEMENT**

Sir:

In accordance with 37 C.F.R. §§ 1.97 and 1.98, it is requested that the following references, which are also listed on the attached Form PTO-1449, be made of record in the above-identified case.

1. Press W.H. et al., "Numerical Recipes in C", Cambridge University Press (1992);
2. Davidson A.R. et al., "Folded Proteins Occur Frequently in Libraries of Random Amino Acid Sequences", Proc. Natl. Acad. Sci USA 91:2146-2150 (1994);
3. Park B.H. et al., "The Complexity and Accuracy of Discrete State Models of Protein Structure", J. Mol. Biol. 249:493-507 (1995);

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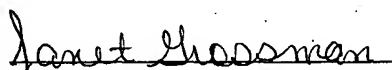
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I hereby certify that this correspondence is being deposited with the United States Postal Service Express Mail Post Office to Addressee service under 37 C.F.R. §1.10 on the date indicated above and is addressed to the Assistant Commissioner of Patents and Trademarks, Washington, D.C. 20231.

Dated: January 31, 2002

  
Janet Grossman

4. Flower D.R., "SERF: A Program for Accessible Surface Area Calculations", J. Mol. Graphics Mod. 15:238-244 (1997);
5. MacKenzie K.R. et al., "A Transmembrane Helix Dimer: Structure and Implications", Science 276:131-133 (1997);
6. Dahiyat B.I. et al., "De Novo Protein Design: Fully Automated Sequence Selection", Science 278:82-87 (1997);
7. Li H. et al., "Are Protein Folds Atypical?", Proc. Natl. Acad. Sci. USA 95:4987-4990 (1998);
8. Harbury P.B. et al., "High-Resolution Protein Design with Backbone Freedom", Science 282:1462-1467 (1998);
9. Gordon D.B. et al., "Energy Functions for Protein Design", Current Opinion in Structural Biology 9:509-513 (1999);
10. Vita C. et al., "Rational Engineering of a Miniprotein that Reproduces the Core of the CD4 site interacting with HIV-1 Envelope Glycoprotein", PNAS 96(23):13091-13096 (1999);
11. Liang S. et al., "Construction of Protein Binding Sites in Scaffold Structures", Biopolymers 54:515-523 (2000);
12. Nakajima N. et al., "Free Energy Landscapes of Peptides by Enhanced Conformational Sampling", J. Mol. Biol. 296:197-216 (2000);
13. Brown S. et al., "A Genetic Analysis of Crystal Growth", J. Mol. Biol. 299:725-735 (2000); and
14. Keefe A.D. et al., "Functional Proteins from a Random-Sequence Library", Nature 410:715-718 (2001).

Applicants are submitting copies of the above-cited references.

Inasmuch as this Information Disclosure Statement is being submitted in accordance with the schedule set out in 37 C.F.R. § 1.97(b), no statement or fee is required.

Respectfully submitted,



Paul J. Esatto, Jr.

Registration No. 30,749

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PIB/PJE:dg

Form PTO-1449 U.S. DEPARTMENT OF COMMERCE (REV. 7-80) PATENT AND TRADEMARK OFFICE		<b>Atty. Docket No. (Optional)</b> 15157	<b>Application Number</b> Unassigned
<b>LIST OF PRIOR ART CITED BY APPLICANT</b>  <i>(Use several sheets if necessary)</i>		<b>Applicant(s)</b> Eldon Emberly, et al.	
		<b>Filing Date</b> Herewith	<b>Group Art Unit</b> Unassigned
		<b>OTHER DOCUMENTS</b> <i>(Including Author, Title, Date, Pertinent Pages, Etc.)</i>	
		Dahiyat B.I. et al., "De Novo Protein Design: Fully Automated Sequence Selection", <u>Science</u> <b>278</b> :82-87 (1997)	
		Li H. et al., "Are Protein Folds Atypical?", <u>Proc. Natl. Acad. Sci. USA</u> <b>95</b> :4987-4990 (1998)	
		Harbury P.B. et al., "High-Resolution Protein Design with Backbone Freedom", <u>Science</u> <b>282</b> :1462-1467 (1998)	
		Gordon D.B. et al., "Energy Functions for Protein Design", <u>Current Opinion in Structural Biology</u> <b>9</b> :509-513 (1999)	
		Vita C. et al., "Rational Engineering of a Miniprotein that Reproduces the Core of the CD4 site interacting with HIV-1 Envelope Glycoprotein", <u>PNAS</u> <b>96</b> (23):13091-13096 (1999)	
		Liang S. et al., "Construction of Protein Binding Sites in Scaffold Structures", <u>Biopolymers</u> <b>54</b> :515-523 (2000)	
		Nakajima N. et al., "Free Energy Landscapes of Peptides by Enhanced Conformational Sampling", <u>J. Mol. Biol.</u> <b>296</b> :197-216 (2000)	
		Brown S. et al., "A Genetic Analysis of Crystal Growth", <u>J. Mol. Biol.</u> <b>299</b> :725-735 (2000)	
		Keefe A.D. et al., "Functional Proteins from a Random-Sequence Library", <u>Nature</u> <b>410</b> :715-718 (2001)	
<b>EXAMINER</b>		<b>DATE CONSIDERED</b>	
* EXAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609; draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.			

Form PTO-1449  
(REV. 7-80) U.S. DEPARTMENT OF COMMERCE  
PATENT AND TRADEMARK OFFICE**LIST OF PRIOR ART  
CITED BY APPLICANT***(Use several sheets if necessary)*

Atty. Docket No. (Optional)

15157

Applicant Number

Unassigned

Applicant(s)

Eldon Emberly, et al.

Filing Date

Herewith

Group Art Unit

Unassigned

JC#28 U.S. PTO  
10/066496**U.S. PATENT DOCUMENTS**

EXAMINER INITIAL*		DOCUMENT NUMBER	DATE	NAME	CLASS	SUBCLASS	FILING DATE (if appropriate)
	AA						
	AB						
	AC						
	AD						

**FOREIGN PATENT DOCUMENTS**

	REF	DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUBCLASS	TRANSLATION	
							YES	NO

**OTHER DOCUMENTS** *(Including Author, Title, Date, Pertinent Pages, Etc.)*

		Press W.H. et al., "Numerical Recipes in C", <u>Cambridge University Press</u> (1992)
		Davidson A.R. et al., "Folded Proteins Occur Frequently in Libraries of Random Amino Acid Sequences", <u>Proc. Natl. Acad. Sci USA</u> 91:2146-2150 (1994)
		Park B.H. et al., "The Complexity and Accuracy of Discrete State Models of Protein Structure", <u>J. Mol. Biol.</u> 249:493-507 (1995)
		Flower D.R., "SERF: A Program for Accessible Surface Area Calculations", <u>J. Mol. Graphics Mod.</u> 15:238-244 (1997)
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